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CHARACTER CORRELATION AND PATH COEFFICIENT IN SOYBEAN *GLYCINE MAX* (L.) MERRILL

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Abstract

Thirty-three soybean genotypes were evaluated for days to flowering, days to maturity, pod length, number of branches, number of unfilled, filled pods and total pods, 100 seed weight and seed yield. Grain yield (kg ha^{-1}) was estimated on the basis of 12 m^2 plot size. Genetic parameters, correlation, path coefficients and linkage distances were estimated for all these traits. Analysis of variance and mean performance for yield and its components revealed significant differences among all the genotypes for all the characters. Seed weight had positive correlation with unfilled, filled and total pods. Grain yield had positive and significant correlation with all the characters except days to flowering and seed yield per 5 plant. Moreover, it had significant but negative correlation with days to maturity and also negatively correlated with un-filled pods. Days to maturity, branches, pod length, pods and 100 seed weight had positive direct effects on grain yield. High indirect effect was also exhibited via pod length by most of the traits hence these characters may be given more emphasis while selecting high yield soybean lines. Cluster diagram based on Euclidean dissimilarity revealed three clusters at 50% linkage distance, cluster I consisted 14 genotypes, cluster II 8 and cluster III 11 genotypes. The accessions in the cluster III were of short duration and high yielding having high seed weight.

Introduction

Soybean (*Glycine max* (L) Merrill) of the family Leguminosae is considered a miracle crop due to its extraordinary qualities. In Pakistan, it is one of the non-conventional oilseed crop that can be successfully grown during spring as well as the summer season. It contains 40 to 42% good quality protein and 18 to 22% oil comprising 85% unsaturated fatty acids and is free from cholesterol alongwith ample mineral elements, so it is highly desirable in human diet. The seeds leftover after solvent extraction are ground to make high protein meal which is used largely as a supplement to cereal seeds in feed for poultry and dairy/beef animals. Being legume it also fixes atmospheric nitrogen to available form. As the best source of protein it truly claims the title “the meat that grows on plant”. Although soybean as an oil crop was introduced in Pakistan 1970’s along with sunflower, but it could not make its place in the country. Even after 3 decades it could not get popularized among farmer. Probably, the main reasons of this are the lack of genetic and breeding work, unavailability of genotypes suitable for different cropping patterns.

The knowledge of certain genetic parameters is essential for proper understanding and their manipulation in any crop improvement programme. Grain yield is the result of the expression and association of several plant growth components. Correlation coefficients, although useful in quantifying the size and direction of trait associations, can be misleading if the high correlation between two traits is a consequence of the indirect effect of the traits (Dewey & Lu, 1959). In soybean, scientists used path analysis, which partitions the genotypic correlations into direct and indirect effects of the traits (Ali *et al*., 1989; Shivashankar & Viswanatha, 1989; Akhter & Sneller, 1996; Board *et al*., 1997; Taware *et al*., 1997; Shukla *et al*., 1998; Board *et al*., 1999; Iqbal *et al*., 2003), whereas, Ghafoor *et al*., (1990); Yadev *et al*., (2001); Arshad *et al*., (2003); Ghafoor *et al*., (2003) and Arshad *et al*., (2004) have mentioned the worth of this techniques in other legumes also.

Keeping in view the importance of this technique the present study was planned to investigate the genetic parameter, correlation coefficient and path analysis alongwith genetic traits to identify the best genotypes on the basis of results for future exploitation.

Materials and Methods

Thirty-three advance soybean genotypes as mentioned in the cluster diagram of different origin were planted in a Randomized Complete Block Design (RCBD) with 3 replications during the year 2003-04 at the National Agricultural Research Center (NARC), Islamabad, Pakistan. The experiment had plot size measuring an area of 12 m^2 having 4 rows of 5 meter length of each genotype. Row to row and plant to plant distance were maintained at 30 and 10 cm, respectively. Sowing was done with the help of hand drill to ensure proper seed depth and to maintain desired plant population in a specific area. All recommended cultural practices were followed uniformly that helps for healthy crop growth as recommended by Kale (1985). After emergence of seedling, thinning was done to maintain the optimum plant population. Five randomly sampled plants were picked up for recording data of selected parameters. These parameters includes days to 50% flowering, days to physiological maturity, pod length (cm), number of branches plant^{-1}, number of unfilled pods plant^{-1}, number of filled pods plant^{-1}, total number of pods plant^{-1}, 100 seed weight, 5 plant yield (gm) and grain yield (kg ha^{-1}).

The average data were subjected to standard statistical techniques for analysis of variance to test the significance level of variation among the genotypes for different characters according to Steel & Torrie, (1980). Genetic parameters, correlation coefficients were computed according to the method suggested by Singh & Chaudhry (1979). The significance of genotypic correlation coefficients was tested with the help of standard errors as suggested by Reeve & Rao (1981). Path coefficients were worked out by the methods used by Dewey & Lu (1959), whereas, genetic distances were calculated from mean with the help of computer software '*Statistica* for Windows' using WARDS method (Sneath & Sokal, 1973). All the three clusters were also analysed for mean and SD.

Results and Discussion

The results regarding of variance and genetic parameters (mean, range, genotypic and phenotypic variance, standard deviation, heritability and genetic advance for ten characters are presented in the Table 1. The results revealed significant differences among all the genotypes for all the characters under this study whereas replication differences were insignificant that revealed high acceptance of the results. Similarly, low differences between genotypic and phenotypic variance for most of characters indicated negligible environmental effects. Malik (2002) and Rasaily *et al*., (1986) also reported similar results for number of pods plant^{-1}, branches plant^{-1} and unfilled pod plant^{-1} in soybean.

High heritability coupled with high genetic advance for days to flowering and pod length revealed the importance of additive gene action that could be exploited through simple selection due to high range of both these traits (Table 1). Although, grain yield kg ha^{-1} also exhibited high heritability and genetic advance but due to estimated yield in kg ha^{-1}, this statistics may be misleading because similar pattern was not observed for grain yield plant^{-1}. For most of the characters where low heritability and genetic advance was observed there is a need to build a broad based germplasm through collection and acquisition (Iqbal *et al*., 2003).

Correlation coefficient study

The genotypic correlation coefficients were higher as compared to phenotypic and environmental correlation coefficient in most of the cases (Table 2). This indicates greater contribution of genotypic factor in the development of the character associations. Significantly, positive genotypic correlation of days to flowering with pod length (0.452**) and unfilled pods (0.318) were observed. However, negative genotypic correlation of days to flowering with five plants yield (-0.707**) was also observed that is suggested to be broken through various breeding techniques to develop short duration high yielding cultivar to fit in various cropping pattern. Similarly, negative association of days to maturity with 100 seed weight (-0.457**) and grain yield (-0.345*) suggested the same phenomenon. Positive genotypic correlation of days to maturity with branches plant^{-1} (0.047) unfilled and filled pods and total pods plant^{-1} were also observed but were non significant. Pod length had significant and positive genotypic correlation with unfilled (0.488**), filled (0.486**) and total pods (0.505**), 100 seed weight (0.393*) and grain yield (0.980**). Rajput *et al*., (1986) and Yao *et al*., (1987) also reported similar results of correlation between pods plant^{-1} and grain yield. According to Malhotra *et al*., (1972) the results of correlation among branches plant^{-1} and pods plant^{-1} with grain yield were similar as presented in this study but 100 seed weight results did not agree.

Grain yield had highly significant positive genotypic correlation with pod length (0.980**), number of branches (0.499**), number of filled (0.670**) and total pods (0.665**) and 100 seed weight (0.788**) while days to flowering (0.259) and 5 plant yield (0.139) had also positive but non significant genotypic correlation with grain yield. Positive and strong association of pod length, branches plant^{-1}, number of pods plant^{-1} and 100 seed weight with grain yield revealed importance of these characters in determining grain yield. Khanghah & Sohani (1999) Rajanna *et al*., (2000) and Singh & Yadava (2000) also reported similar findings for different parameters in soybean. According to Siahsar & Rezai (1999) number of pod plant^{-1} had the greatest genotypic correlation with seed yield in soybean which also confirms the results of present investigation. The negative associations of characters like days to maturity and un-filled pods will become problem in combining these important traits in a single genotype for high grain yield. Some suitable recombination might be obtained through bi-parental mating, mutation breeding or diallel selective mating by breaking undesirable linkage as suggested by Ghafoor *et al*., (1990).

Table 4. Mean and standard deviation of three cluster for 10 variables.

Variables	Mean ± SD		
	Cluster I	Cluster II	Cluster III
Days to flowering	48.36±3.46	45.46±2.44	43.61±1.58
Days to maturity	99.71±3.41	98.00±1.62	95.76±2.34
5 PodslLength	16.86±2.33	13.65±1.54	16.41±1.97
Branches	4.67±0.83	3.82±0.64	3.94±0.41
Un-filled pods	0.62±0.13	0.49±0.06	0.58±0.09
Filled pods	16.19±1.45	13.24±1.34	15.51±2.08
Total pods	16.81±1.43	13.74±1.33	16.08±2.07
100 Seed weight	21.43±2.68	20.62±2.35	23.88±1.28
5 Plant yield	14.69±2.37	16.03±4.13	20.82±2.61
Grain yield	1256.44±454.10	702.84±408.69	1325.28±212.65

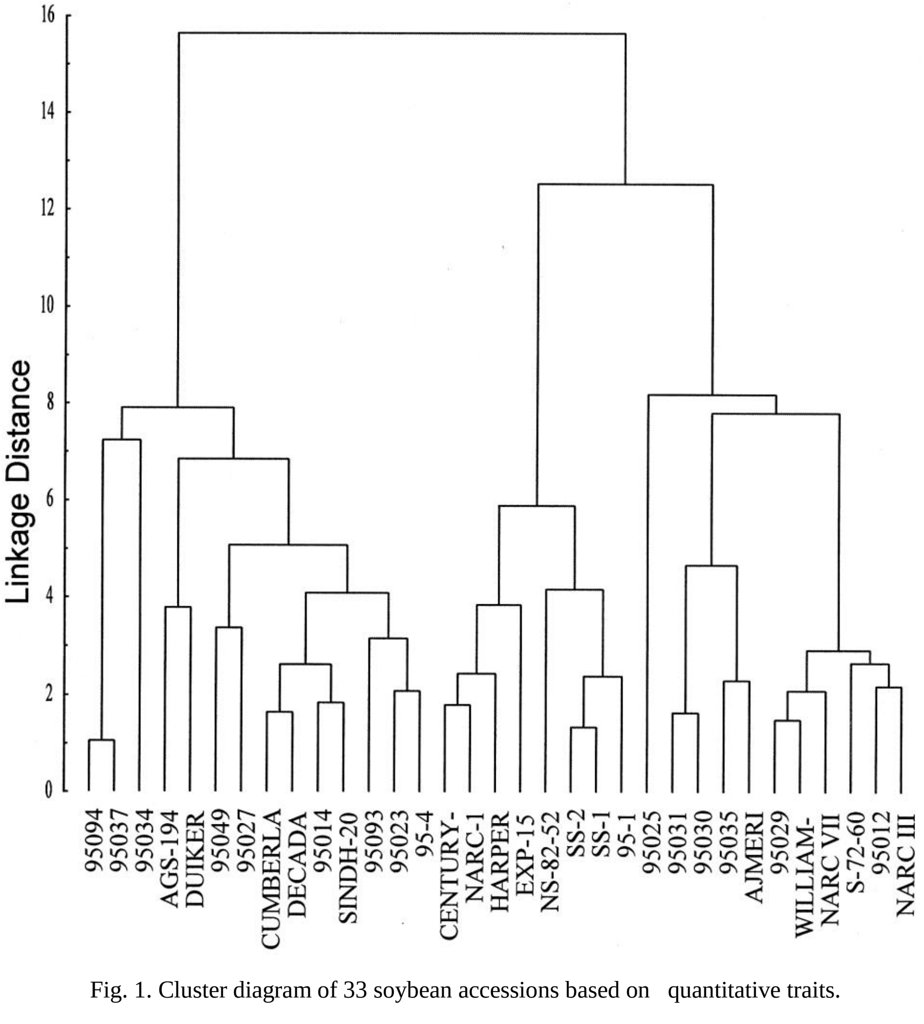

Fig. 1. Cluster diagram of 33 soybean accessions based on quantitative traits.

Path coefficient study

The result of genotypic correlation coefficients was partitioned into direct and indirect effects through various yield contributing characters (Table 3). The direct effects of days to maturity, branches plant^{-1}, pod length, number of pods plant^{-1} and 100 seed weight were positive while the remaining characters exhibited negative direct effects. The highest direct effect was exhibited by pods plant^{-1} and it was followed by pod length. These results were confirmed by Khan *et al*., (2000); Singh & Yadava (2000) and Shrivastava *et al*., (2001) in soybean. The direct effects of days to maturity and 100 seed weight ratio were also positive. Yadev *et al*., (2001); Ashraf *et al*., (2002) and Arshad *et al*., (2004) also observed similar type of results in their studies conducted on urdbean, wheat and chickpea. As their was no irrigation applied to this experiment hence the whole crop was grown under rainfed condition indicated that pod length, number of pods and 100 seed weight had maximum contribution in determining grain yield in soybean. It was also observed that high indirect contribution was also exhibited *via* pod length, number of pods plant^{-1} and 100 seed weight hence these three traits may be given more emphasis while selecting high yielding soybean lines for rainfed agriculture. The results were also confirmed by Ball *et al*., (2001).

Cluster diagram based on Euclidean dissimilarity using Ward's method revealed three clusters at 50% linkage distance, cluster I consisted 14 genotypes, cluster II eight and cluster III consisted 11 genotypes. There was no clear indication observed on the basis of origin of genotypes (Fig. 1). All the three clusters were analysed for mean and SD (Table 4). It is evident from the results that the accessions in the cluster III i.e., NARC III, NARC VII, S-72-60, Ajmeri, William-82, 95012, 95025, 95029, 95030, 95031 and 95035 were short duration and high yielding having high seed weight. Therefore, these genotypes could be tested under wider range of environments.

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